In the Claims:

1. (Currently Amended) A computer system ~~A method~~ for identifying a drug discovery target, the system comprising:

~~(a)~~ ~~providing~~ a computer ~~for storing and accessing genomics information~~ comprising a database to store and access genomics information ~~wherein said computer permits computational analysis of biological relationships among the stored genomics information,~~ wherein said genomics information is stored as an ontology;

wherein the computer system is configured to:

(a) perform computational analysis of biological relationships among the stored genomics information

(b) query[[ing]] the database to identify [[a]] disease-related pathways; and

(c) identify[[ing]] the biological objects and processes that act on those objects in the disease-related pathways whereby each object or process involved in the disease-related pathways is a drug discovery target~~; and~~

~~(d) accessing displaying the drug discovery target[[s]] to a user~~.

2. (Currently Amended) The computer system ~~method~~ of claim 1 wherein the genomics information comprises information relating to genes, their DNA sequences, their mRNA, proteins expressed from said genes, and the biological effects of the expressed proteins.

3. (Currently Amended) The computer system ~~method~~ of claim 2 wherein said genomics information comprises data extracted from multiple public sources.

4. (Currently Amended) The computer system ~~method~~ of claim 2 wherein said genomics information comprises proprietary data.

5. (Currently Amended) The computer system ~~method~~ of claim 2 wherein said genomics information comprises data extracted from a combination of proprietary and public data sources.

6. (Cancelled)

7. (Currently Amended) The computer system ~~method~~ of claim 2 wherein ~~the means for storing the genomics information includes an~~ the ontology is organized so that ~~in which~~:

(a) each gene, ~~gene product~~ mRNA, protein expressed from said gene, and biological effect is given an identifier which is related to synonyms for the identifier;

(b) each gene, ~~gene product~~ mRNA, protein expressed from said gene, and biological effect is categorized by class; and

(c) the relationship of each gene, ~~gene product~~ mRNA, protein expressed from said gene and disease state is defined by slots and facets.

8. (Currently Amended) The computer system ~~method~~ of claim [[2]] 1 wherein drug discovery targets in the disease related pathway are prioritized based on factors that include function and complexity.

9. (Currently Amended) The computer system ~~method~~ of claim [[8]] 1 wherein drug discovery targets are ~~further~~ prioritized based on markers for side effects and patient responsiveness.

10-12. (Cancelled)

13. (Currently Amended) The computer system ~~method~~ of claim 1 wherein the genomics information comprises information relating to genotype and the disease-related pathway comprises a gene, mRNA or protein expressed from said gene associated with a particular genotype.

14. (Currently Amended) The computer system ~~method~~ of claim 1 wherein the genomics information comprises the name of each gene, mRNA or protein expressed from said gene, and their biological effects, and the ~~means for storing and accessing the genomics information~~ computer identifies relationships between genes and/or proteins expressed from said genes that are at least two steps removed from each other in a disease-related pathway.

15-61. (Cancelled)

62. (New) The computer system of claim 1, further comprising a second database for a knowledge base of scientific findings.

63. (New) The computer system of claim 62, wherein the knowledge base is a frame-based knowledge base.

64. (New) The computer system of claim 1, wherein the system is further configured to compare disease-related pathways with data obtained from gene expression studies or a manually entered gene list.

65. (New) The computer system of claim 64, wherein the gene expression studies comprise differential gene expression studies or microarray studies.

66. (New) The computer system of claim 64, wherein the comparison of the disease-related pathways with user-defined data is made using a statistical model.

67. (New) The computer system of claim 66, wherein the statistical model calculates the probability that overlaps between disease-related pathways and user-defined data is a random event.

68. (New) The computer system of claim 1, wherein the identification step further comprises storing the identified biological objects and processes according to the ontology.

69. (New) The computer system of claim 1, wherein performance of computational analysis of biological relationships among the stored genomics information comprises generating one or more subsets of genomics information.

70. (New) The computer system of claim 69, wherein the one or more subsets of genomics information are pre-generated from the database.

71. (New) The computer system of claim 69, wherein the one or more subsets of genomics information are generated by one of a data-driven and model-driven approach.

72. (New) The computer system of claim 69, wherein the one or more subsets of genomics information are generated based upon information contained in the database and user supplied genomics information.

73. (New) The computer system of claim 69, further comprising the step of providing a user-supplied set of gene expression data for identifying a particular subset of genomics information, wherein the gene expression data are selected based on one or more of expression levels derived from microarray experiments, a prior analysis algorithm, and a user's preferred gene set.

74. (New) The computer system of claim 69, wherein the one or more subsets of genomics information are gene-centric being derived about a central gene for all genes in the database.

75. (New) The computer system of claim 69, wherein the generation of one or more subsets of genomics information further comprises deriving one or more subsets of genomics information of related user-selected genes.

76. (New) The computer system of claim 76, wherein the one or more subsets of genomics information are generated so as to be non-overlapping by ensuring that user-selected genes do not appear in more than a predetermined maximum threshold number of subset of genomics information.

77. (New) The computer system of claim 76, wherein the one or more subsets of genomics information are generated so as to be based on connections between a first known drug target gene and a second drug target gene of interest.

78. (New) A networked computer system for identifying a drug discovery target comprising:

a communication network; and

a computer system coupled to the communication network comprising a database for storing and accessing genomics information;

wherein the computer system is configured to:

(a) perform computational analysis of biological relationships among the stored genomics information;

(b) query the database to identify a disease-related pathway; and

(c) identify the biological objects and processes that act on those objects in the disease-related pathway whereby each object or process involved in the disease-related pathway is a drug discovery target.